IN THE CLAIMS:

1. (currently amended) A method for the determination of cellular lipid individual molecular species composition of matter in a biological sample, said method comprising:

subjecting the biological sample to lipid extraction to obtain a lipid extract;

subjecting the lipid extract to two dimensional electrospray ionization tandem mass spectrometry (ESI/MS/MS);

~~to generate~~generating a two dimensional plot representing molecular ions of the lipid extract on a first axis and at least one of neutral loss scans of fatty acids of the lipid extract and precursor ion scans on a second axis; and

comparing peak heights for the molecular ions with that for an internal standard to at least one of identify and quantify the lipid molecular species.

2. (previously presented) A method in accordance with Claim 1 wherein the lipid extract is obtained via at least one of a chloroform lipid extraction, a chloroform/ methanol extraction, and a butanol extraction.

3. (previously presented) A method in accordance with Claim 1 wherein said extraction is of at least one of a blood, serum, tissue, tissue biopsy, feces and urine sample.

4. (previously presented) A method in accordance with Claim 1 wherein said biological sample is at least one of a mammalian tissue, a plant tissue, a microbiological sample, and a fungal sample.

5. (previously presented) A method in accordance with Claim 4 wherein the mammalian tissue is human tissue and the lipid is at least one of a triacylglyceride, a phospholipid, and any other lipid species contained within biologic membranes.

6. (previously presented) A method in accordance with Claim 1 further comprising determining a fingerprint profile of a lipid individual molecular species.

7. (previously presented) A method in accordance with Claim 6 wherein said fingerprint profile represents the individual molecular species of a lipid composition of matter.

8. (currently amended) A method for the determination of cellular lipid individual molecular species composition of matter directly from a lipid extract of a biological sample, said method comprising:

subjecting said lipid extract to electrospray ionization tandem mass spectrometry;

~~to generate~~generating a two dimensional plot of molecular ions of the lipid extract versus at least one of neutral loss scans and precursor ion scans of lipid classes of the lipid extract; and

comparing peak heights for the molecular ions with that for an internal standard to identify and/or quantify the lipid molecular species.

9. (previously presented) A method in accordance with Claim 8 wherein said lipid extract is obtained via at least one of chloroform extraction, a chloroform/ methanol extraction, and a butanol extraction.

10. (previously presented) A method in accordance with Claim 8 wherein said biological sample is at least one of a mammalian and a plant tissue.

11. (original) A method in accordance with Claim 10 wherein said mammalian tissue is human tissue.

12. (previously presented) A method in accordance with Claim 8 wherein the biological sample is an aqueous human fluid sample subjected to at least one of centrifugation and conventional column chromatography suitable for separation of lipoproteins to resolve lipids into different lipoprotein fractions.

13. (previously presented) A method in accordance with Claim 12 wherein the aqueous human fluid sample is at least one of whole blood, blood serum, blood plasma, liver and urine.

14. (previously presented) A method in accordance with Claim 13 wherein the lipid extract is obtained by extraction of said biological sample with at least one of chloroform and any other solvent.

15. (previously presented) A method in accordance with Claim 8 wherein said internal standard includes a control sample of lipid molecular species.

16. (previously presented) A method in accordance with Claim 8 further comprising at least one of iteratively deconvoluting and normalizing the peak heights for the molecular ions.

17. (previously presented) A method in accordance with Claim 8 further comprising deconvoluting the intensity of two dimensional intercept contours of at least one of the neutral loss scans and the precursor ion scans for multidimensional mass spectrometry.

18-54. (canceled)

55. (currently amended) A method in accordance with Claim 1 wherein said lipid comprises at least one of phospholipids ~~(e.g., choline glycerophospholipides (e.g., plasmenycholine, phosphatidylcholine, plasmanylcholine), sphingomeyelin, ethanolamine glycerophospholipids, mono and dimethyl ethanolamine, glycerophospholipds, serine glycerophospholipids, inositol glycerophospholipids, cardiolipin, phosphatidic acid, phosphatidylglycerol, phasphatidylethanol and oxidized derivatives thereof)~~, fatty acids, fatty amides, eicosanoids, sphingolipids, glycolipids, steroids, ceramides, acylCoA, acylcarnitine, acylprotiens, acylpeptides, diglycerides, monoglycerides, anadamide and 2-arachidonyl glycerol or oxidized nitrated or sulfated species therefrom or other derivatives know to those in the field.

56. (canceled).

57. (new) A method in accordance with Claim 55 wherein said phospholipid is selected from the group consisting of choline glycerophospholipids, sphingomeyelin, ethanolamine glycerophospholipids, mono and dimethyl ethanolamine, glycerophospholipds, serine glycerophospholipids, inositol glycerophospholipids, cardiolipin, phosphatidic acid, phosphatidylglycerol, phasphatidylethanol and oxidized derivatives thereof.

58. (new) A method in accordance with Claim 57 wherein said choline glycerophospholipids are selected from the group consisting of plasmenycholine, phosphatidylcholine, and plasmanylcholine.